

Mapping Project"

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ORIGIN
Query Match      7.3%; Score 411.8; DB 6; Length 868;
Best Local Similarity 97.6%; Pred. No. 2.2e-94;
Matches 439; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

QY 3645 GGTGCAAGTCAACAGAGTACTAGCAATGTTACGGTGCACTGCCCTACCTCAAGT 3704
DB 415 GGTGCAAGTCAACAGAGTACTAGCAATGTTACGGTGCACTGCCCTACCTCAAGT 474
QY 3705 GAATAGGAAGCAAACTGAGAGTACGTGCTTCAAAAAATCAATTAAGTTTCGTTCCAC 3764
DB 475 GAATAGGAAGCAAACTGAGAGTACGTGCTTCAAAAAATCAATTAAGTTTCGTTCCAC 534
QY 3765 CAAATTGTAATTTTGTGTATCTTCCACTGATATTTCTTCAAAAAATCAATTAAGTTTCGTTCCAC 3824
DB 535 CAAATTGTAATTTTGTGTATCTTCCACTGATATTTCTTCAAAAAATCAATTAAGTTTCGTTCCAC 594
QY 3825 TTCAAGCAAA--GCAAAAAAACAATCCTGGTATCAACAGTATAGCATATTTTCAAGATGA 3882
DB 595 TTCAAGCAAGGGGGGAGACAATCTTGGTATCAACAGTATAGCATATTTTCAAGATGA 654
QY 3883 GGTGCACTGCTTGTATAGTTGTTATTTAGTCGCAAAATATGTGCAAGTAAGAGTGGCACT 3942
DB 655 GGTGCACTGCTTGTATAGTTGTTATTTAGTCGCAAAATATGTGCAAGTAAGAGTGGCACT 714
QY 3943 TGAGCCATTAGCTCTCTTAGGATATAGCCAGAGATCGTGTATATGCTGTGCAAGACA 4002
DB 715 TGAGCCATTAGCTCTCTTAGGATATAGCCAGAGATCGTGTATATGCTGTGCAAGACA 774
QY 4003 CTGTTTTCACCAATTTATATATAGCTGCAATGTTTACATGATCAAGCTTGAATAGGA 4062
DB 775 CTGTTTTCACCAATTTATATATAGCTGCAATGTTTACATGATCAAGCTTGAATAGGA 834
QY 4063 TATGGGATGAGTGCAACTGCTGGAGATAGC 4092
DB 835 TATGGGATGAGTGCC-ACTGCTGGAGATACC 863

RESULT 11
A1374506/c 871 bp mRNA linear EST 21-JAN-1999
LOCUS MEST6-D3.POLYT-N.Seq ISUM2 Zea mays cDNA clone MEST6-D3 5', mRNA
DEFINITION MEST6-D3.POLYT-N.Seq ISUM2 Zea mays cDNA clone MEST6-D3 5', mRNA
sequence.
ACCESSION A1374506
VERSION A1374506.1 GI:4174526
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
Wen, T.J., Ashlock, D.A. and Schnable, P.S.
Expressed Sequence Tags from B73 Maize Seedlings
Unpublished (1997)
Contact: Schnable, PS
Schnable Laboratory
Iowa State University
G405 Agronomy, Ames, IA 50011, USA
Tel: (515)-294-0975
Fax: (515)-294-2299
Email: schnable@iastate.edu
PCR Primers
FORWARD: tw1412 (5'-GAAGATACCCCAACCAACC-3')
BACKWARD: T7-YJ (5'-TAATACCACTCACTATAGGC-3')
Plate: MEST6 row: D column: 3
Seq primer: POLYT-N (5'-TTTTTTTTTTTTTTTTTTTTTTT (AGC)-3').
Location/Qualifiers
1..871
/organism="Zea mays"
/mol_type="mRNA"

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/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST6-D3"
/tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="XLI-MFR Blue"
/clone_lib="ISUM2"
/notes="Organ: green seedlings; Vector: pAD-GAL4; Site 1:
ECORI; Site 2: XhoI; ds-cDNA molecules were generated as
follows. First-strand cDNA was prepared from oligo-dT
selected mRNA by priming with an XhoI oligo-dT primer. The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcorI adaptors, the
ds-cDNAs were digested with XhoI and size-selected. The
resulting molecules were directionally cloned into the
ECORI and XhoI sites of the HybriZAP lambda vector
(Stratagene) and excised as pAD-GAL4 phagemids."

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ORIGIN

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Query Match      7.3%; Score 410; DB 1; Length 871;
Best Local Similarity 99.5%; Pred. No. 6.4e-94;
Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3645 GGTGCAAGTCAACAGAGTACTAGCAATGTTACGGTGCACTGCCCTACCTCAAGT 3704
DB 428 GGTGCAAGTCAACAGAGTACTAGCAATGTTACGGTGCACTGCCCTACCTCAAGT 369
QY 3705 GAATAGGAAGCAAACTGAGAGTACGTGCTTCAAAAAATCAATTAAGTTTCGTTCCAC 3764
DB 368 GAATAGGAAGCAAACTGAGAGTACGTGCTTCAAAAAATCAATTAAGTTTCGTTCCAC 309
QY 3765 CAAATTGTAATTTTGTGTATCTTCCACTGATATTTCTTCAAAAAATCAATTAAGTTTCGTTCCAC 3824
DB 308 CAAATTGTAATTTTGTGTATCTTCCACTGATATTTCTTCAAAAAATCAATTAAGTTTCGTTCCAC 249
QY 3825 TTCAAGCAAGCAAAACAACTCCTGGTATCAACAGTATAGCATATTTTCAAGATGAGG 3884
DB 248 TTCAAGCAAGCAAAACAACTCCTGGTATCAACAGTATAGCATATTTTCAAGATGAGG 189
QY 3885 TGCACCTGCTTATAGTTGTTATTTAGTCGCAATATGTCAGTATAGCTGGCCTTG 3944
DB 188 TGCACCTGCTTATAGTTGTTATTTAGTCGCAATATGTCAGTATAGCTGGCCTTG 129
QY 3945 AGCCATTAGCTCCTTTAGGATATGGCAGCAGATCGTGTATATGCTGTGCAAGACT 4004
DB 128 AGCCATTAGCTCCTTTAGGATATGGCAGCAGATCGTGTATATGCTGTGCAAGACT 69
QY 4005 GTTTTGCAACCAATTTATATATAGCTGCAATGTTTACATGATGAAGCTTGAATAGGATA 4064
DB 68 GTTTTGCAACCAATTTATATATAGCTGCAATGTTTACATGATGAAGCTT-AAAATAGGATA 10
QY 4065 TGG 4067
DB 9 TGG 7

RESULT 12
CW239849/c 685 bp DNA linear GSS 30-OCT-2004
LOCUS CW239849.1 GI:54948676
DEFINITION 104 698 11217883 116 37521 076 Sorghum bicolor genomic clone 11217883, genomic survey
sequence.
ACCESSION CW239849
VERSION CW239849.1
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,

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Db 459 GGTTCGGGTGACGGGAGGGGCAAGATCGTGGCGGTGCGCGGAGGAGCAGCACCTGC 400
 Qy 361 TCGCAAGAAGAACACCAAGCGCAAGAGAGGCTCTCGAAGATGGTCAAGTCAACCAAGA 420
 Db 399 TCGCAAGAAGAACACCAAGCGCAAGAGAGGCTCTCGAAGATGGTCAAGTCAACCAAGA 340
 Qy 421 GTGACTAGCAAGTGTACGGGTGCACCTGCGCTACCTCAAGTGAATAGGAAGCAAACT 480
 Db 339 GTGACTAGCAAGTGTACGGGTGCACCTGCGCTACCTCAAGTGAATAGGAAGCAAACT 280
 Qy 481 GAGAGCTACGTGCTCTTCAAAAAAATCATTAAGTTTCGTTCCACCAAAATTTGTAATTTGTG 540
 Db 279 GAGAGCTACGTGCTCTTCAAAAAAATCATTAAGTTTCGTTCCACCAAAATTTGTAATTTGTG 220
 Qy 541 TATCTTCACGTGATTTCTTCTCAAAAAATCACTGAGGCATCATTTCAAGCAAGCAAAAA 600
 Db 219 TATCTTCACGTGATTTCTTCTCAAAAAATCACTGAGGCATCATTTCAAGCAAGCAAAAA 160
 Qy 601 ACACTCTCGTATCAACAGTATAGCATATTTTCCAGATGAGTGCACCTGCTGTATAG 660
 Db 159 ACACTCTCGTATCAACAGTATAGCATATTTTCCAGATGAGTGCACCTGCTGTATAG 100
 Qy 661 TTGTTATTTAGTCCCAATATGTGCAAGTAAAGTGGCAGTTCGAGCCATTAGCTCCTCTT 720
 Db 99 TTGTTATTTAGTCCCAATATGTGCAAGTAAAGTGGCAGTTCGAGCCATTAGCTCCTCTT 44
 Qy 721 AGGATATGGCCAGCAGATCGTGTATATGGCTGTGCAAGACACT 763
 Db 43 AGGATATGGCCAGCAGATCGTGTATATGGCTGTGCAAGACACT 1

RESULT 3
 AI374506/c
 LOCUS
 DEFINITION
 sequence.
 AI374506
 AI374506.1 GI:4174526
 EST.

ORGANISM
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 871)
 Wen, T. J., Ashlock, D. A. and Schnable, P. S.
 Expressed Sequence Tags from B73 Maize Seedlings
 Unpublished (1997)
 Contact: Schnable, PS
 Iowa State University
 Schnable laboratory
 G405 Agronomy, Ames, IA 50011, USA
 Tel: (515)-294-0975
 Fax: (515)-294-2299
 Email: schnable@iastate.edu

PCR Primers
 FORWARD: tw1412 (5'-GAAGATACCCCAACCAACC-3')
 BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGC-3')
 Plate: MEST6 row: D column: 3
 Seq primer: POLYT-N (5'-TTTTTTTTTTTTTTTTTTTTTTT (AGC)-3').

FEATURES

Location/Qualifiers
 1..871
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone="MEST6-D3"
 /tissue_type="above ground tissues"
 /dev_stage="Two-leaf-stage green seedling"
 /lab_host="XLI-MPR Blue"
 /clone_lib="ISUM2"
 /note="Organ: green seedlings; Vector: PAD-GAL4; Site 1:
 EcoRI; Site 2: XhoI; ds-cDNA molecules were generated as

follows. First-strand cDNA was prepared from oligo-dT
 selected mRNA by priming with an XhoI oligo-dT primer. The
 resulting DNA:RNA hybrid was treated with RNase H and used
 as a template for DNA PolI-catalyzed second strand
 synthesis. After the addition of EcoRI adaptors, the
 ds-cDNAs were digested with XhoI and size-selected. The
 resulting molecules were directionally cloned into the
 EcoRI and XhoI sites of the HybriZAP lambda vector
 (Stratagene) and excised as PAD-GAL4 phagemids."

ORIGIN

Query Match 80.7%; Score 672; DB 1; Length 871;
 Best Local Similarity 96.7%; Pred. No. 1.3e-162;
 Matches 703; Conservative 0; Mismatches 22; Indels 2; Gaps 2;
 Qy 100 CCGCGCAGGAGCCAGGAAGCTACCCGACGACGCTCGCATTTCCCGCGCAAACTCTTCT 159
 Db 731 CCGCGGCGAGNAGCAGGAAGTACCC-CAGCCAGCCTNGCATTCGCGGGAATCCTTTT 673
 Qy 160 TCGCGCGCGCTGGCGCGCCACCGCGGCTCCGTCGCGTCCGCTCCCGCGCAAGCGG 219
 Db 672 TGGGNGCGCGCTTGGCGCGCCACCGCGGCTTCNGTCGGGTGCGCGTCCCGCGCAAGCGG 613
 Qy 220 CCACCTCCACCACTCGCTCGAGTCTCGCGGCGGGAAGAGGCTACAGATGAAGA 279
 Db 612 CCACCTCCACCACTTCGTTAGAGGTCTGTCGCGCGGGAAGAGGCTACAGATGAAGA 553
 Qy 280 CGCACAAAGGCGTCGGCGAAGCGGTTCCGGGTGACGGGAGGGGCAAGATCTGCGGCGGT 339
 Db 552 CGCACAAAGGCGTCGGCGAAGCGGTTCCGGGTGACGGGAGGGGCAAGATCTGCGGCGGT 493
 Qy 340 GCGCGCGGGAAGCAGCACTTCTCGCCAAAGAAACACCAAGCGCGCAAGAGGCTCTCGA 399
 Db 492 GCGCGGGAAGCAGCACTTCTCGCCAAAGAAACACCAAGCGCGCAAGAGGCTCTCGA 433
 Qy 400 AGATGTGCAAGTCAACAAGAGTGACTACGACAAATGTTACGGGTGCACTGCCCTACCTCA 459
 Db 432 AGATGTGCAAGTCAACAAGAGTGACTACGACAAATGTTACGGGTGCACTGCCCTACCTCA 373
 Qy 460 AAGTGAATAGCAAGCAAACTGAGAGCTACGTGCTTCAAAAAATCATTTAAGTTTCGTT 519
 Db 372 AAGTGAATAGCAAGCAAACTGAGAGCTACGTGCTTCAAAAAATCATTTAAGTTTCGTT 313
 Qy 520 CCACCAAAATGTAATTTTGTATCTTCCACTGTATTTCTTCTTCAAAAAATCTAGAGCA 579
 Db 312 CCACCAAAATGTAATTTTGTATCTTCCACTGTATTTCTTCTTCAAAAAATCTAGAGCA 253
 Qy 580 TCATTTCAAGCAAGCAAAAAACAATCTCTGTTATCAACAGTATAGCGATATTTTCAGAT 639
 Db 252 TCATTTCAAGCAAGCAAAAAACAATCTCTGTTATCAACAGTATAGCGATATTTTCAGAT 193
 Qy 640 GAGTGCACCTGCTGTATAGTTGTTATTTAGTCGCAAAATATGCAAGTAAAGAGTGCA 699
 Db 192 GAGTGCACCTGCTGTATAGTTGTTATTTAGTCGCAAAATATGCAAGTAAAGAGTGCA 133
 Qy 700 CTTGAGCCATTAGCTCCTCTTAGGATATGCCAGCAGATCGTGTATATGGCTGTGCAAGA 759
 Db 132 CTTGAGCCATTAGCTCCTCTTAGGATATGCCAGCAGATCGTGTATATGGCTGTGCAAGA 73
 Qy 760 CACTGTTTGCACCATTTATATATAGCTGCATTTGTTACATGATGAAGCTTGAATAG 819
 Db 72 CACTGTTTGCACCATTTATATATAGCTGCATTTGTTACATGATGAAGCTTGAATAG 14
 Qy 820 GATATGG 826
 Db 13 GATATGG 7

RESULT 4
 AI001298
 LOCUS
 DEFINITION

AI001298 803 bp mRNA linear EST 05-JUN-1998
 MEST6-D3.TW1412.Seq ISUM2 Zea mays cDNA clone MEST6-D3 5', mRNA
 sequence.